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Search for

=====

Welcome to the SIB BLAST Network Service

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In case of problems, please read the [online BLAST help](#).
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

=====

Query: 30 AA

Date run: 2005-10-27 21:09:24 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

2,482,761 sequences; 813,543,939 total letters

UniProt Knowledgebase Release 6.3 consists of:

UniProtKB/Swiss-Prot Release 48.3 of 25-Oct-2005: 196277 entries

UniProtKB/TrEMBL Release 31.3 of 25-Oct-2005: 2273976 entries

List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db AC	Description	Score E-value
<input type="checkbox"/> tr Q83U44	_CLOPE Beta2-toxin [cpb2] [Clostridium perfringens]	95 2e-19
<input type="checkbox"/> tr Q4ZFT7	_CLOPE Beta2 toxin [Clostridium perfringens]	95 2e-19
<input type="checkbox"/> tr Q4ZFT6	_CLOPE Beta2 toxin [Clostridium perfringens]	95 2e-19
<input type="checkbox"/> tr Q86264	_CLOPE Beta 2 toxin precursor [Clostridium perfringens C]	95 2e-19
<input type="checkbox"/> tr Q93MD0	_CLOPE Beta2-toxin [cpb2] [Clostridium perfringens]	89 1e-17
<input type="checkbox"/> tr Q4ZFT4	_CLOPE Beta2 toxin [Clostridium perfringens]	88 3e-17
<input type="checkbox"/> tr Q50NG8	_ENTHI Receptor protein kinase, putative [442.t00003] [...]	48 3e-05
<input type="checkbox"/> tr Q72MW1	_LEPIC Hypothetical protein [LIC13078] [Leptospira inte...]	36 0.083
<input type="checkbox"/> tr Q4AAS7	_MYCHJ Signal peptidase I (EC 3.4.21.89) [sipS] [Mycopl...]	35 0.20

<input type="checkbox"/>	tr	Q5HX88	_CAMJR Cytolethal distending toxin, subunit C [cdtC] [C...	35	0.27
<input type="checkbox"/>	tr	Q46102	_CAMJE CdtC (Cytolethal distending toxin C) [cdtC] [Cam...	35	0.27
<input checked="" type="checkbox"/>	tr	Q7B3S5	_CAMJE CdtC protein (Fragment) [cdtC] [Campylobacter je...	35	0.27
<input type="checkbox"/>	tr	Q5F1K4	_CAMJE Cytolethal distending toxin C [cdtC] [Campylobac...	35	0.27
<input type="checkbox"/>	tr	Q33865	_BACPU Plasmid pSH1452, Rep [Bacillus pumilus (Bacillus...	35	0.27
<input type="checkbox"/>	sp	P04660	HEMA_IADNY Hemagglutinin precursor [Contains: Hemagglu...	34	0.48
<input type="checkbox"/>	tr	Q81L65	_BACAN Iron compound ABC transporter, iron compound-bin...	34	0.48
<input type="checkbox"/>	tr	Q894Q1	_CLOTE Membrane associated protein [CTC01484] [Clostrid...	33	0.87
<input type="checkbox"/>	tr	Q4A8Y6	_MYCH7 Signal peptidase I (EC 3.4.21.89) [sipS] [Mycopl...	33	0.87
<input type="checkbox"/>	tr	Q54JE1	_DICDI Hypothetical protein [DDB0187788] [Dictyostelium...	32	1.2
<input type="checkbox"/>	tr	Q52TF1	_CAMJE Cytolethal distending toxin C (Fragment) [cdtC] ...	32	1.6
<input type="checkbox"/>	tr	Q52TF0	_CAMJE Cytolethal distending toxin C (Fragment) [cdtC] ...	32	1.6
<input type="checkbox"/>	sp	P45963	ACR7_CAEL Acetylcholine receptor, alpha-type subunit ...	32	2.1
<input type="checkbox"/>	tr	Q8EZK0	_LEPIN Hypothetical protein [LA3853] [Leptospira interr...	32	2.1
<input type="checkbox"/>	tr	Q731T5	_BACC1 HlyC domain protein [BCE4080] [Bacillus cereus (...]	32	2.1
<input type="checkbox"/>	tr	Q41GQ2	_9BACI Binding-protein-dependent transport systems inne...	32	2.1
<input type="checkbox"/>	tr	Q59092	_PYRHO Hypothetical protein PH1367 [PH1367] [Pyrococcus...	32	2.1
<input type="checkbox"/>	tr	Q8TID2	_METAC Predicted protein [MA4221] [Methanosarcina aceti...	32	2.1
<input type="checkbox"/>	sp	Q98KB0	MRAY_RHILO Phospho-N-acetylmuramoyl-pentapeptide-trans...	31	2.8
<input type="checkbox"/>	tr	Q8AWN0	_9SMEG Rhodopsin (Fragment) [Rhod] [Spinachia spinachia]	31	2.8
<input type="checkbox"/>	tr	Q7YTK2	_CAEEL Hypothetical protein [W01D2.6] [Caenorhabditis e...	31	2.8
<input type="checkbox"/>	tr	Q4IBS5	_GIBZE Hypothetical protein [FG05333.1] [Gibberella zea...	31	2.8
<input type="checkbox"/>	sp	P87245	KMS1_SCHPO Karyogamy meiotic segregation protein 1 [km...	31	3.8
<input type="checkbox"/>	tr	Q897V9	_CLOTE Hypothetical protein [CTC00614] [Clostridium tet...	31	3.8
<input type="checkbox"/>	tr	Q488C5	_COLP3 Arylsulfatase (EC 3.1.6.1) [atsA] [Colwellia psy...	31	3.8
<input type="checkbox"/>	tr	Q4YW58	_PLABE Hypothetical protein [PB000503.02.0] [Plasmodium...	31	3.8
<input type="checkbox"/>	tr	Q4XSE9	_PLACH Hypothetical protein [PC000754.03.0] [Plasmodium...	31	3.8
<input type="checkbox"/>	tr	Q45280	_CAEEL Hypothetical protein srbc-83 [srbc-83] [Caenorha...	31	3.8
<input type="checkbox"/>	tr	Q6CS24	_KLULA Similar to sp P25371 Saccharomyces cerevisiae YC...	31	3.8
<input type="checkbox"/>	tr	Q3T6M7	_9PERO Rhodopsin (Fragment) [Archoplites interruptus]	30	5.1
<input type="checkbox"/>	tr	Q3T6M3	_9PERO Rhodopsin (Fragment) [Enneacanthus obesus]	30	5.1
<input type="checkbox"/>	tr	Q3QJ06	_9GAMM Protein-disulfide reductase precursor (EC 1.8.1....	30	5.1
<input type="checkbox"/>	tr	Q3NFU5	_9HELI Cytochrome c, class I precursor [TmdenDRAFT_1375...	30	5.1
<input type="checkbox"/>	tr	Q5ZGC8	_9VIRU Transmembrane glycoprotein [PHG11b_49] [Bacterio...	30	5.1
<input type="checkbox"/>	tr	Q61RZ6	_CAEBR Hypothetical protein CBG06382 [CBG06382] [Caenor...	30	5.1
<input type="checkbox"/>	tr	Q6YMD9	_9HEMI Cytochrome oxidase subunit I (Fragment) [COI] [L...	30	5.1
<input type="checkbox"/>	tr	Q50SK5	_ENTHI Hypothetical protein [256.t00009] [Entamoeba his...	30	5.1
<input type="checkbox"/>	tr	Q8U1W2	_PYRFU Hypothetical protein PF1092 [PF1092] [Pyrococcus...	30	5.1
<input type="checkbox"/>	tr	Q91F76	_IRV6 450L [Chilo iridescent virus (CIV) (Insect irides...	30	6.8
<input type="checkbox"/>	tr	Q8QLT2	_9INFA Non structural protein 1 [NS1] [Influenza A viru...	30	6.8
<input type="checkbox"/>	tr	Q8Y8R0	_LISMO Putative peptidoglycan bound protein (LPXTG moti...	30	6.8
<input type="checkbox"/>	tr	Q6HR76	_BACAN Hypothetical protein [BAS4921] [Bacillus anthracis]	30	6.8
<input type="checkbox"/>	tr	Q4EVA3	_LISMO Cell wall surface anchor family protein [LMOf685...	30	6.8
<input type="checkbox"/>	tr	Q6C7M8	_YARLI Similar to sp P38778 Saccharomyces cerevisiae Tr...	30	6.8
<input type="checkbox"/>	tr	Q4SLL1	_TETNG Chromosome 15 SCAF14556, whole genome shotgun se...	29	9.1

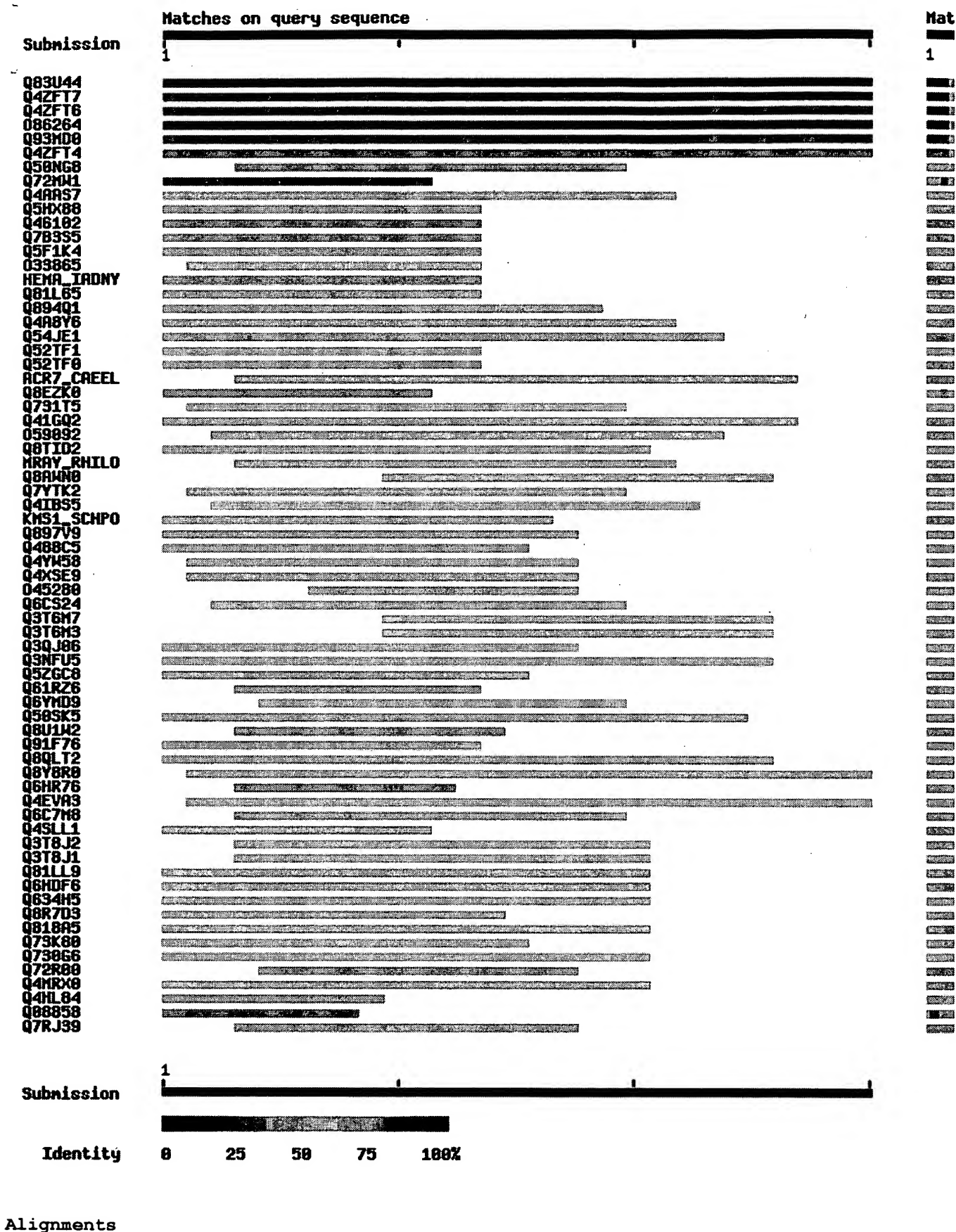
<input type="checkbox"/>	tr Q3T8J2	_9NIDO Polyprotein lab [pollab] [Breda virus]	29	9.1
<input type="checkbox"/>	tr Q3T8J1	_9NIDO Replicase [ORF1a] [Breda virus]	29	9.1
<input type="checkbox"/>	tr Q81LL9	_BACAN Iron compound ABC transporter, iron compound-bin...	29	9.1
<input type="checkbox"/>	tr Q6HDF6	_BACHK Iron compound ABC transporter, iron compound-bin...	29	9.1
<input type="checkbox"/>	tr Q634H5	_BACCZ Iron compound ABC transporter, iron compound-bin...	29	9.1
<input type="checkbox"/>	tr Q8R7D3	_THETN Membrane-associated lipoprotein involved in thia...	29	9.1
<input type="checkbox"/>	tr Q818A5	_BACCR Ferrichrome-binding protein [BC4363] [Bacillus c...	29	9.1
<input type="checkbox"/>	tr Q73K80	_TREDE FMN-binding domain protein [TDE2340] [Treponema ...	29	9.1
<input type="checkbox"/>	tr Q730G6	_BACC1 Iron compound ABC transporter, iron compound-bin...	29	9.1
<input type="checkbox"/>	tr Q72R00	_LEPIC Hypothetical protein [LIC11952] [Leptospira inte...	29	9.1
<input type="checkbox"/>	tr Q4MRX0	_BACCE Ferrichrome-binding protein [BCE_G9241_4421] [Ba...	29	9.1
<input type="checkbox"/>	tr Q4HL84	_CAMLA Hypothetical protein [CLA0484] [Campylobacter la...	29	9.1
<input type="checkbox"/>	tr Q08858	_KLEPN Fimbrial adhesin precursor [fimH] [Klebsiella pn...	29	9.1
<input type="checkbox"/>	tr Q7RJ39	_PLAYO Hypothetical protein [PY03425] [Plasmodium yoeli...	29	9.1

Graphical overview of the alignments

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Profile hits

Pfam hits



tr Q83U44 Beta2-toxin [cpb2] [Clostridium perfringens] 265 AA
Q83U44_CLOPE
[align](#)

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

Query: 1 MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1 MKKIISKFTVIFMFSCFLIVGAISPMKASA 30

tr Q4ZFT7 Beta2 toxin [Clostridium perfringens] 265 AA
Q4ZFT7_CLOPE
[align](#)

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

Query: 1 MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1 MKKIISKFTVIFMFSCFLIVGAISPMKASA 30

tr Q4ZFT6 Beta2 toxin [Clostridium perfringens] 265 AA
Q4ZFT6_CLOPE
[align](#)

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

Query: 1 MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1 MKKIISKFTVIFMFSCFLIVGAISPMKASA 30

tr O86264 Beta 2 toxin precursor [Clostridium perfringens C] 265 AA
O86264_CLOPE
[align](#)

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

Query: 1 MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1 MKKIISKFTVIFMFSCFLIVGAISPMKASA 30

tr Q93MD0 Beta2-toxin [cpb2] [Clostridium perfringens] 265 AA
Q93MD0_CLOPE
[align](#)

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UniProtKB/Swiss-Prot entry P09870

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[\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	CLOS_CLOHI
Primary accession number	P09870
Secondary accession number	P09869
Entered in Swiss-Prot in	Release 10, March 1989
Sequence was last modified in	Release 26, July 1993
Annotations were last modified in	Release 49, January 2006
Name and origin of the protein	
Protein name	Alpha-clostripain [Precursor]
Synonyms	EC 3.4.22.8 Clostridiopeptidase B
Contains	Alpha-clostripain light chain Alpha-clostripain heavy chain
Gene name	Name: cloSI
From	Clostridium histolyticum [TaxID: 1498]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

- [1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
DOI=10.1007/BF00276893; PubMed=8341259 [NCBI, ExPASy, EBI, Israel, Japan]
Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;
"The heterodimeric protease clostripain from Clostridium histolyticum is encoded by a single gene.";
Mol. Gen. Genet. 240:140-145(1993).
- [2] PROTEIN SEQUENCE OF 51-181.
PubMed=6391922 [NCBI, ExPASy, EBI, Israel, Japan]
Gilles A.M., Lecroisey A., Keil B.;
"Primary structure of alpha-clostripain light chain.";
Eur. J. Biochem. 145:469-476(1984).
- [3] PRELIMINARY PROTEIN SEQUENCE OF 51-73 AND 191-232.
PubMed=6337850 [NCBI, ExPASy, EBI, Israel, Japan]
Gilles A.M., de Wolf A., Keil B.;
"Amino-acid sequences of the active-site sulfhydryl peptide and other thiol peptides from the cysteine proteinase alpha-clostripain.";
Eur. J. Biochem. 130:473-479(1983).

Comments

- **FUNCTION:** Cysteine endopeptidase with strict specificity.
- **CATALYTIC ACTIVITY:** Preferential cleavage: Arg-|-Xaa, including Arg-|-Pro bond, but not Lys-|-Xaa.
- **SUBUNIT:** Heterodimer of a light chain and an heavy chain held together by strong noncovalent forces rather than by intramolecular disulfide bridges.
- **SIMILARITY:** Belongs to the peptidase C11 family [view classification].
- **DATABASE:** NAME=Worthington enzyme manual; WWW="http://www.worthington-biochem.com/CP/".

Copyright

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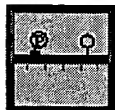
Cross-references

EMBL	X63673; CAA45212.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A29174; A29174. A29175; A29175. B29175; B29175. S35190; S35190.	
MEROPS	C11.001; -.	
InterPro	IPR005077; Peptidase_C11. Graphical view of domain structure.	
Pfam	PF03415; Peptidase_C11; 1. Pfam graphical view of domain structure.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
BLOCKS	P09870.	
ProtoNet	P09870.	
ProtoMap	P09870.	
PRESAGE	P09870.	
DIP	P09870.	
ModBase	P09870.	
SWISS-2DPAGE	Get region on 2D PAGE.	
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.	

Keywords

Direct protein sequencing; Hydrolase; Protease; Signal; Thiol protease; Zymogen.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FTId
SIGNAL	1	27	27	Potential.	
PROPEP	28	50	23	Potential.	PRO_0000028511
CHAIN	51	181	131	Alpha-clostripain light chain.	PRO_0000028512
PROPEP	182	190	9	Linker.	PRO_0000028513
CHAIN	191	526	336	Alpha-clostripain heavy chain.	PRO_0000028514

ACT_SITE 231 231
 CONFLICT 127 127 R -> NQL (in Ref. 2).
 CONFLICT 176 179 HGGG -> GDGH (in Ref. 2).
 CONFLICT 197 197 S -> H (in Ref. 3).
 CONFLICT 213 213 I -> L (in Ref. 3).
 CONFLICT 216 216 H -> T (in Ref. 3).
 CONFLICT 232 232 L -> M (in Ref. 3).

Sequence information

Length: **526 AA** [This is the length of the unprocessed precursor]

Molecular weight: **59733 Da** [This is the MW of the unprocessed precursor]

CRC64: **E151372FF6C95BE7** [This is a checksum on the sequence]

```

      10      20      30      40      50      60
MLRRKVSTLL MTALITTSFL NSKPVYANPV TSKDNNLKE VQVTSKSNK NKNQKVTIMY

      70      80      90     100     110     120
YCDADNNLEG SLLNDIEEMK TGYKDSPNLN LIALVDRSPR YSSDEKVLGE DFSDTRLYKI

     130     140     150     160     170     180
EHNKANRLDG KNEFPEISTT SKYEANMGDP EVLKKFIDYC KSNYEADKYV LIMANHGGGA

     190     200     210     220     230     240
REKSNPRLNR AICWDDSNLD KNGEADCLYM GEISDHLTEK QSVDLLAFDA CLMGTAEVAY

     250     260     270     280     290     300
QYRPGNGGFS ADTLVASSPV VWGPGFKYDK IFDRIKAGGG TNNEDDLTLG GKEQNFDPAT

     310     320     330     340     350     360
ITNEQLGALF VEEQRDSTHA NGRYDQHLSF YDLKKAESVK RAIDNLAVNL SNENKKSEIE

     370     380     390     400     410     420
KLKRGSIHTD LMHYFDEYSE GEWVEYPYFD VYDLCEKINK SENFSSKTKD LASNAMNKLN

     430     440     450     460     470     480
EMIVYSFGDP SNNFKEGKNG LSIFLPNGDK KYSTYYTSTK IPHWTMQSWY NSIDTVKYGL

     490     500     510     520
NPYGKLSWCK DGQDPEINKV GNWFELLD SW FDKTNDVTGG VNHYQW
  
```

P09870 in FASTA format

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 ExPASy/SIB
 or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
 Compute pI/Mw, PeptideMass, PeptideCutter,
 Dotlet (Java)



ScanProsite, MotifScan




Submit a homology modeling request to SWISS-MODEL



NPSA Sequence analysis tools

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Entry Information

Entry from: [EMBL](#)

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☒

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General Information

Primary Accession # X63673

Accession # X63673

Entry Name EMBL:CHCLOSI

Molecule Type genomic DNA

Sequence Length 2768

Entry Division PRO

Sequence Version X63673.1

Creation Date 21-FEB-1992

Modification Date 19-JUL-1993

Description

Description C.histolyticum closI gene for alpha-clostripain

Keywords closI gene; Clostripain.;

Organism Clostridium histolyticum

Organism Classification Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae

References

1. Diefenthal,T.;

Submitted (28-JAN-1992) to the EMBL/GenBank/DDBJ database
Research, Dept. Biotechnology, Schaarstr.1, P.O.B. 20 65,
Position 1-2368

2. Dargatz,H.; Diefenthal,T.; Witte,V.; Reipen,G.; von Wettst
The heterodimeric protease clostripain from Clostridium
single gene

Mol. Gen. Genet. 240(1):140-145 (1993)

DOI [10.1007/BF00276893](#)

Pubmed [8341259](#)

Position 1-2368

Additional Information

Features

Key	Location	Qualifier	Value
<u>source</u>	1..2768	db_xref	<u>taxon:1498</u>
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		organism	Clostridium histolyti
<u>-35_signal</u>	376..381		
<u>-10_signal</u>	397..402		
<u>repeat_region</u>	420..438	note	palindrom-structure
		rpt_type	INVERTED
<u>rbs</u>	605..609		
<u>cds</u>	618..2198	db_xref	<u>GOA:P09870</u>
		db_xref	<u>InterPro:IPR0050</u>
		db_xref	<u>UniProtKB/Swiss-I</u>
		transl_table	11
		gene	ClosI
		EC_number	<u>3.4.22.8</u>
		product	clostripain
		protein_id	<u>CAA45212.1</u>
		translation	>CAA45212 MLRRKVSTLLMTAL YCDADNNLEGSLNI EHNKANRLDGKNEFI REKSNPRLNRAICWI

Sequence

Characteristics **Length:** 2768 BP, **A Count:**1084, **C Count:**359, **G Count**
Sequence

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Go to: [General](#) [Description](#) [References](#) [Additional](#) [Sequence](#)

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Entry Information

Entry from: [EMBL features](#)

ID CHCLOSI_2; parent: [CHCLOSI](#)
AC X63673;
FT -35_signal 376..381
SQ Sequence 6 BP;
ttgtaa

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Entry Options

Launch analysis tool:

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information:[Link](#)

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Entry Information

Entry from: [EMBL features](#)

Entry Options

Launch analysis tool:

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information:[Link](#)

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[Save](#)

View:

[Printer Friendly](#)

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SQ  Sequence            6 BP;
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Entry Information

Entry from: [EMBL features](#)

Entry Options

Launch analysis tool:

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[Save](#)

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[Printer Friendly](#)

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 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 24-JAN-2006 (Rel. 49, Last annotation update)
 DE Alpha-clostripain precursor (EC 3.4.22.8) (Clostridiopeptidase B)
 DE [Contains: Alpha-clostripain light chain; Alpha-clostripain heavy
 DE chain].
 GN Name=cloSI;
 OS Clostridium histolyticum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
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 RN [1]
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 RX MEDLINE=93341452; PubMed=8341259; DOI=10.1007/BF00276893;
 RA Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;
 RT "The heterodimeric protease clostripain from Clostridium histolyticum
 RT is encoded by a single gene.";
 RL Mol. Gen. Genet. 240:140-145(1993).
 RN [2]
 RP PROTEIN SEQUENCE OF 51-181.
 RX MEDLINE=85076641; PubMed=6391922;
 RA Gilles A.M., Lecroisey A., Keil B.;
 RT "Primary structure of alpha-clostripain light chain.";
 RL Eur. J. Biochem. 145:469-476(1984).
 RN [3]
 RP PRELIMINARY PROTEIN SEQUENCE OF 51-73 AND 191-232.
 RX MEDLINE=83131688; PubMed=6337850;
 RA Gilles A.M., de Wolf A., Keil B.;
 RT "Amino-acid sequences of the active-site sulfhydryl peptide and other
 RT thiol peptides from the cysteine proteinase alpha-clostripain.";
 RL Eur. J. Biochem. 130:473-479(1983).
 CC -!- FUNCTION: Cysteine endopeptidase with strict specificity.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, including
 CC Arg-|-Pro bond, but not Lys-|-Xaa.
 CC -!- SUBUNIT: Heterodimer of a light chain and an heavy chain held
 CC together by strong noncovalent forces rather than by
 CC intramolecular disulfide bridges.
 CC -!- SIMILARITY: Belongs to the peptidase C11 family.
 CC -!- DATABASE: NAME=Worthington enzyme manual;
 CC WWW="http://www.worthington-biochem.com/CP/".
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; X63673; CAA45212.1; -; Genomic_DNA.
 DR PIR; A29174; A29174.
 DR PIR; A29175; A29175.
 DR PIR; B29175; B29175.
 DR PIR; S35190; S35190.
 DR MEROPS; C11.001; -.
 DR InterPro; IPR005077; Peptidase_C11.
 DR Pfam; PF03415; Peptidase_C11; 1.
 KW Direct protein sequencing; Hydrolase; Protease; Signal;
 KW Thiol protease; Zymogen.
 FT SIGNAL 1 27 Potential.

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FT                                     /FTid=PRO_0000028512.
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FT  CHAIN      191     526     Alpha-clostripain heavy chain.
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FT  CONFLICT   176     179     HGGG -> GDGH (in Ref. 2).
FT  CONFLICT   197     197     S -> H (in Ref. 3).
FT  CONFLICT   213     213     I -> L (in Ref. 3).
FT  CONFLICT   216     216     H -> T (in Ref. 3).
FT  CONFLICT   232     232     L -> M (in Ref. 3).
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      EHNKANRLDG KNEFPEISTT SKYEANMGDP EVLKKFIDYC KSNYEADKYV LIMANHGGGA
      REKSNPRLNR AICWDDSNLD KNGEADCLYM GEISDHLTEK QSVDLLAFDA CLMGTAEVAY
      QYRPGNGGFS ADTLVASSPV VWGPGFKYDK IFDRIKAGGG TNNEDDLTLG GKEQNFDPAT
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      KLRGSGIHDT LMHYFDEYSE GEWVEYPYFD VYDLCEKINK SENFSSKTKD LASNAMNKLN
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Entry Information

Entry from: [EMBL features](#)

Entry Options

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information:

Save entry:

View:

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AC      L77965;
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SV      L77965.1
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DT      28-JUL-1998 (Rel. 56, Created)
DT      29-JUL-1998 (Rel. 56, Last updated, Version 2)
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OC      Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC      Clostridium.
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RP      1-1392
RX      DOI; 10.1016/S0378-1119(97)00493-9
RX      PUBMED; 9426008.
RA      Gibert M., Jolivet-Reynaud C., Popoff M.R.;
RT      "Beta2 toxin, a novel toxin produced by Clostridium perfringens";
RL      Gene 203(1):65-73(1997).
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RN      [2]
RP      1-1392
RA      Popoff M.R.;
RT      ;
RL      Submitted (15-JAN-1998) to the EMBL/GenBank/DDBJ databases.
RL      Toxines Microbiennes, Institut Pasteur, Paris cedex 15 75724, France
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CC      [Flatfile retrieved from GSDB Fri Jul 24 15:39:17 1998].
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